

**Amendments to the Specification**

Please replace the paragraph at page 9, lines 1-26, with the following amended paragraph.

By way of example, hBVR of SEQ. ID. No. 1 is characterized by a number of functional domains, including putative and/or demonstrated phosphorylation sites from aa 15 to 20, aa 21 to 23, aa 44 to 46 or 47, aa 49 to 54, aa 58 to 61, aa 64 to 67, aa 78 to 81, aa 79 to 82, aa 189 to 192, aa 207 to 209, aa 214 to 217, aa 222 to 227, aa 236 to 241, aa 245 to 250, aa 267 to 269 or 270, and aa 294 to 296; a basic N-terminal domain characterized by aa 6 to 8; a hydrophobic domain characterized by aa 9 to 14 (FXVVVV, SEQ. ID. No. 6); a nucleotide binding domain characterized by aa 15 to 20 (GXGXXG, SEQ. ID. No. 7); an oxidoreductase domain characterized by aa 90 to 97 (AGLHVLVE AGKHLVLE, SEQ. ID. No. 8); a leucine zipper spanning aa 129 to 157 (LX<sub>6</sub>LX<sub>6</sub>KX<sub>6</sub>LX<sub>6</sub>L, SEQ. ID. No. 9); several kinase motifs, including aa 44 to 46 (SRR, SEQ. ID. No. 10), aa 147 to 149 (KGS, SEQ. ID. No. 11) and aa 162 to 164 (FTX FGX, SEQ. ID. No. 12); a nuclear localization signal spanning aa 222 to 228 (GLKRNRY, SEQ. ID. No. 13); a myristylation site spanning aa 221 to 225 (PGLKR, SEQ. ID. No. 14); a zinc finger domain spanning aa 280 to 293 (HCX<sub>10</sub>CC, SEQ. ID. No. 15); and substrate binding domains including, without limitation, a protein kinase C ("PKC") enhancing domain spanning aa 275 to 281 (KKRIXHC, SEQ. ID. No. 16) and a PKC inhibiting domain spanning aa 290 289 to 296 (QKXCXXXK, SEQ. ID. No. 17). By way of sequence comparison and, in consideration of conserved substitutions, hBVR of SEQ. ID. No. 3 and rBVR of SEQ. ID. No. 4 include similar functional domains. For example rBVR includes an identical hydrophobic domain, an identical nucleotide binding domain, an identical oxidoreductase domain, a conserved leucine zipper domain (with residue variations between L and K residues), identical or conserved kinase motifs, an identical nuclear localization signal, an identical myristylation site, a conserved zinc finger domain (with terminal C residue replaced by H), a conserved PKC enhancing domain, and a conserved PKC inhibiting domain.

**Amendments to the Sequence Listing**

Please replace the sequence listing of record in this application with the accompanying corrected sequence listing. In particular, the corrected sequence listing contains corrections to SEQ ID NOS: 8 and 12.